

AMENDMENTS TO THE CLAIMS:

This listing of the claims below will replace all prior versions and listing of claims in this application.

1. (Currently Amended) A genetically Genetically modified plant cell, characterised in that it has having an increased activity of at least one Class 3 branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified.
2. (Currently Amended) The genetically Genetically modified plant cell according to Claim 1, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant genetically modified plant cell comprises at least one foreign nucleic acid molecule that has been introduced into the genome of the plant cell.
3. (Currently Amended) The genetically Genetically modified plant cell according to Claim 2, wherein the foreign nucleic acid molecule codes a Class 3 branching enzyme.
4. (Currently Amended) The genetically Genetically modified plant cell according to Claim 3, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
 - a) a nucleic Nucleie acid molecule molecules, which [[code]] codes a protein with the amino acid sequence given under Seq ID NO 4;
 - b) a nucleic Nucleie acid molecule molecules, which [[code]] codes a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
 - c) a nucleic Nucleie acid molecule molecules, which include includes the nucleotide sequence shown under of Seq ID NO 3 or a complimentary complementary sequence;
 - d) a nucleic Nucleie acid molecule molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
 - e) a nucleic Nucleie acid molecule molecules, which hybridise hybridizes with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
 - f) a nucleic Nucleie acid molecule molecules, the nucleotide sequence of which deviates

from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f)
due to the degeneration of the genetic code; [[and]] or

g) a nucleic ~~Nucleie~~ acid molecule ~~molecules~~, which ~~represent~~ represents fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

5. (Currently Amended) The genetically Genetically modified plant cell according to ~~one of Claims 2 to 4, Claim 2~~, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

a) a T-DNA molecule ~~molecules~~, which ~~lead~~ leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (~~T-DNA activation tagging~~);

b) a DNA molecule ~~molecules~~, which ~~contain~~ contains transposons, which ~~lead~~ leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (~~transposon activation tagging~~);

c) a DNA molecule ~~molecules~~, which [[code]] codes a Class 3 branching enzyme and which are linked with regulatory sequences, which guarantee transcription in vegetable cells and lead to an increase in Class 3 branching enzyme activity in the cell [.] ; or

d) a nucleic ~~Nucleie~~ acid molecule ~~molecules~~ introduced by means of in vivo mutagenesis, which ~~lead~~ leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.

6. (Currently Amended) A plant ~~Plant~~ cell according to ~~one of Claims 1 to 5~~ Claim 1, which synthesises synthesizes a modified starch in comparison with corresponding wild type plant cells that have not been genetically modified.

7. (Currently Amended) A plant ~~Plant~~ containing plant cells according to ~~one of Claims 1 to 6~~ Claim 1.

8. (Currently Amended) A plant ~~Plant~~ according to Claim 7, which is a starch-storing plant.

9. (Currently Amended) A plant Plant according to Claim 7, which is a maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum plant.
10. (Currently Amended) The plant Plant according to Claim 9, which is a potato plant.
11. (Currently Amended) Propagation material of plants according to ~~one of Claims 7 to 10~~
Claim 7, containing plant cells according to one of Claims 1 to 6.
12. (Currently Amended) Harvestable plant parts of plants according to ~~one of Claims 7 to 10~~
Claim 7, containing plant cells according to one of Claims 1 to 6.
13. (Currently Amended) A method Method for the manufacture of a genetically modified plant according to ~~one of Claims 7 to 10~~
Claim 7, wherein comprising
 - a) genetically modifying a plant cell ~~is genetically modified~~, whereby the genetic modification leads to an increase in the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
 - b) regenerating a plant ~~is regenerated~~ from plant cells from Step a); and
 - c) if necessary, producing further plants ~~are produced~~ with the help of the plants according to Step b).
14. (Currently Amended) The method Method according to Claim 13, wherein the genetic modification ~~consists in the comprises~~ introduction of a foreign nucleic acid molecule into the genome of the plant.
15. (Currently Amended) The method Method according to Claim 14, wherein the said foreign nucleic acid molecule is ~~chosen from the group consisting of~~
 - a) a nucleic Nucleic acid molecule molecules, which [[code]] codes a protein with the amino acid sequence ~~given under of~~ Seq ID NO 4;
 - b) a nucleic Nucleic acid molecule molecules, which [[code]] codes a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence ~~given under of~~ SEQ ID NO: 4;

- c) a nucleic acid molecule molecules, which include includes the nucleotide sequence shown under Seq ID NO 3 or a complimentary complementary sequence;
- d) a nucleic acid molecule molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
- e) a nucleic acid molecule molecules, which hybridise hybridizes with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
- f) a nucleic acid molecule molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; [[and]] or
- g) a nucleic acid molecule molecules, which represent represents fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

16. (Currently Amended) The method Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

- a) a T-DNA molecule molecules, which lead leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (T-DNA activation tagging);
- b) a DNA molecule molecules, which contain contains transposons, which lead leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (transposon activation tagging);
- c) a DNA molecule molecules, which [[code]] codes a Class 3 branching enzyme and which are linked with regulatory sequences, which guarantee for transcription in vegetable cells and lead leads to an increase in Class 3 branching enzyme activity in the cell; or
- d) a Nucleic acid molecule molecules introduced by means of in vivo mutagenesis, which lead leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.

17. (Currently Amended) The method Method according to ~~one of Claims 13 to 16~~ Claim 13, wherein the genetically modified plant synthesises synthesizes a modified starch in comparison with corresponding wild type plants that have not been genetically modified.
18. (Currently Amended) A modified Modified starch obtainable from a genetically modified plant according to ~~one of Claims 7 to 10~~ Claim 7, from propagation material according to Claim 11, or from harvestable plant parts according to Claim 12.
19. (Currently Amended) A method Method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to ~~one of Claims 1 to 6~~ Claim 1.
20. (Currently Amended) A method Method for the manufacture of a modified starch including the step of extracting the starch from a plant according to ~~one of Claims 7 to 10~~ Claim 7.
21. (Currently Amended) A method Method for the manufacture of a modified starch including the step of extracting the starch from harvestable plant parts according to Claim 12.
22. (Currently Amended) A method Method for the manufacture of a derived starch, wherein modified starch according to Claim 18 or obtainable by ~~means of a~~ the method according to ~~one of Claims 19, 20 or 21~~ Claim 19 is derived.
23. (Canceled) ~~Use of genetically modified plants according to one of Claims 7 to 10 for the manufacture of a modified starch.~~
24. (Currently Amended) A modified Modified starch obtainable by ~~means of a~~ the method according to ~~one of Claims 19, 20 or 21~~ Claim 19.
25. (Currently Amended) Derived starch obtainable by ~~means of a~~ the method according to Claim 22.
26. (Canceled) ~~Use of modified starch according to one of Claims 18 or 24 for the manufacture of derived starch.~~